**Table S4. Cell cycle parameters from synchronous cultures of LL and NLL homozygous diploid deletion strainsa.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| [**Strain**](http://polywiki.tamu.edu/wiki/bin/view/PolymenisLab/AgingElutriationExperiments?sortcol=0;table=1;up=0#sorted_table) | [**Birth**](http://polywiki.tamu.edu/wiki/bin/view/PolymenisLab/AgingElutriationExperiments?sortcol=4;table=1;up=0#sorted_table)[**size (fL)**](http://polywiki.tamu.edu/wiki/bin/view/PolymenisLab/AgingElutriationExperiments?sortcol=4;table=1;up=0#sorted_table) | ***k*** [**(specific rate of**](http://polywiki.tamu.edu/wiki/bin/view/PolymenisLab/AgingElutriationExperiments?sortcol=3;table=1;up=0#sorted_table)[**size increase (h-1)**](http://polywiki.tamu.edu/wiki/bin/view/PolymenisLab/AgingElutriationExperiments?sortcol=3;table=1;up=0#sorted_table)**)** | [**Critical Size (fL)**](http://polywiki.tamu.edu/wiki/bin/view/PolymenisLab/AgingElutriationExperiments?sortcol=2;table=1;up=0#sorted_table) | [**Estimated**](http://polywiki.tamu.edu/wiki/bin/view/PolymenisLab/AgingElutriationExperiments?sortcol=5;table=1;up=0#sorted_table)[**G1 (TG1, h)**](http://polywiki.tamu.edu/wiki/bin/view/PolymenisLab/AgingElutriationExperiments?sortcol=5;table=1;up=0#sorted_table) |
| **LL** |  |  |  |  |
| *idh2Δ*  | 39.68±2.38 b | **0.221±0.041c** | 62.24±3.64 | 1.72d |
| *hxk2Δ* | **25.93±2.30** | 0.282±0.011 | 65.45±1.66 | 3.06 |
| *lpd1Δ* | **28.86±2.86** | **0.139±0.010** | **54.41±2.21** | 4.5 |
| *tor1Δ* | 43.15±0.14 | **0.248±0.008** | 65.11±3.53 | 1.53 |
| *sch9Δ* | **35.85±0.99** | **0.233±0.020** | 63.24±1.00 | 2.32 |
| *ubr2Δ* | **35.78±2.69** | 0.292±0.016 | **58.00±1.16** | 1.73 |
| *sgf73Δ* | **36.51±1.01** | **0.240±0.016** | **55.28±0.33** | 1.73 |
| *rpp2bΔ* | 40.64±4.09 | 0.299±0.025 | 62.77±1.50 | 1.35 |
| *rei1Δ* | **35.33±2.12** | **0.194±0.024** | 61.2±1.90 | 2.86 |
| *tat2∆* | **37.31±2.01** | 0.301±0.015 | 61.22±2.07 | 1.65 |
| *spt4Δ* | **34.75±1.20** | **0.237±0.017** | 58.73±1.39 | 2.41 |
| *rpl22aΔ* | **32.37±1.31** | **0.219±0.022** | 63.08±2.29 | 2.93 |
| *rpl29Δ* | **37.86±1.54** | **0.231±0.022** | 59.90±1.10 | 2.1 |
| *rpl20bΔ* | **32.80±0.72** | **0.262±0.005** | 60.56±0.97 | 2.25 |
| **NLL** |  |  |  |  |
| BY4743e | 42.12±1.23 | 0.282±0.013 | 61.53±.78 | 1.35 |
| *rps0bΔe* | **34.53±1.89** | **0.238±0.008** | **70.06±1.90** | 2.88 |
| *ylr454wΔ* | 43.87±2.41 | 0.289±0.017 | 61.32±0.98 | 1.35 |
| *tda1Δ* | 41.31±4.95 | 0.282±0.022 | 60.41±1.50 | 1.35 |
| *yal054cΔ* | 40.40±4.09 | 0.285±0.007 | 61.49±1.34 | 1.35 |
| *his7Δ* | 42.52±1.01 | 0.280±0.005 | 61.96±3.08 | 1.35 |
| *rps27bΔ* | 44.29±0.97 | 0.272±0.022 | 62.79±0.71 | 1.35 |
| *sfp1Δe* | **16.04±0.62** | **0.145±0.013** | **39.23±0.0.53** | 6.17 |
| *rpl7bΔ* | 43.05±1.70 | 0.264±0.016 | 60.90±2.10 | 1.35 |
| *rpl34aΔ* | 42.60±0.93 | 0.276±0.038 | 59.94±1.07 | 1.35 |
| *gpa1Δ* | **24.86±0.81** | **0.199±0.008** | **39.10±1.68** | 2.28 |
| *adk1Δ* | **65.29±1.09** | **0.210±0.009** | **102.85±5.73** | 2.1 |
| *dpb4Δf* | **49.92±0.89** | **0.316±0.016** | **64.38±1.08** | 0.82 |

aAll the strains were in the homozygous diploid BY4743 background, and they were examined in YPD (2% Dextrose) medium. All the strains were examined in at least 3 independent experiments, and in each experiment a technical duplicate was evaluated.

bThe average and standard deviation are shown in each case.

cValues shown in bold differ significantly from the same value of the wild type reference strain (p<0.05; unpaired, 2-tail *t* test, assuming unequal variance). The p values associated with each test were calculated with the corresponding function in Microsoft Excel.

dThese are G1 estimates from the formula: G1(hours)=Ln(Critical size/Birth size)/*k*, assuming an exponential mode of growth. Note that these values reflect the G1 length of newborn daughter cells. For G1 length calculations, the errors (± sd) were not propagated, and any parameter that was not significantly different from the same parameter of the wild type reference strain was assigned the wild type value.

eThe values of these strains were obtained from [[48](#_ENREF_48)].

fThe values of this strain were obtained from previously published values (see Hoose SA, Trinh JT, Leitch MC, Kelly MM, McCormick RF, et al. (2013) Saccharomyces cerevisiae deletion strains with complex DNA content profiles. FEMS Microbiol Lett 345: 72-76.)